It is claimed:

1. A method for detecting foreign DNA in a modified host genome, suspected to contain said foreign DNA, which is not present in the unmodified host genome, the method comprising the steps of:

(a) competitively hybridizing first and second populations of polynucleotide probes with a reference DNA population, said reference DNA population comprising DNA sequences characteristic of said foreign DNA, wherein different DNA sequences are attached to separate solid phase supports in clonal subpopulations;

wherein each of said first population of polynucleotide probes comprises a DNA fragment from the unmodified host genome, and has a first label; and each of said second population of polynucleotide probes comprises a DNA fragment from the modified host genome, and has a second, distinguishable label;

thereby forming duplexes between the DNA sequences of the reference DNA population and the polynucleotide probes;

(b) sorting the solid phase supports, according to the ratio of said first label to said second label on the duplexed probes hybridized to each support;

(c) selecting solid phase supports having a ratio of fluorescent signals which falls within a selected range of values different from 1:1; and

(d) identifying the attached sequences or hybridized probes on the selected solid phase supports.

2. The method of claim 1, wherein the first and second labels, respectively, are first and second distinguishable fluorescent labels.

3. The method of claim 1, wherein said solid phase supports are microparticles, and said microparticles are sorted by FACS, according to the ratio of fluorescent signals generated by said fluorescent labels on each microparticle.

4. The method of claim 1, wherein said identifying comprises sequencing at least a portion of said hybridized probes.

5. The method of claim 1, wherein said probe populations are prepared by:

preparing a restriction digest or sheared digest of fragments from said native genome or said modified genome;

ligating pairs of PCR primers to said fragments, wherein each said pair of PCR primers includes at least one labeled primer; and

amplifying said fragments by PCR.

6. The method of claim 1, wherein said probes have a length such that some portion of the first population of probes are able to hybridize with sequences of the reference DNA population, under the conditions of said hybridizing.

7. The method of claim 1, further comprising, prior to step d):

separately hybridizing each said probe population with the reference DNA population;

recovering each said probe population from the solid phase supports; and

amplifying each recovered probe population by PCR, using primers labeled with said first or second labels, respectively.

8. The method of claim 1, further comprising the steps, prior to said competitive hybridization, of:

(i) providing said reference DNA population, comprising DNA sequences characteristic of said foreign DNA, wherein different sequences are attached to separate solid phase supports in clonal subpopulations;

(i) providing said first population of polynucleotide probes, each comprising a DNA fragment from the unmodified host genome, not containing said foreign DNA, and having a first label;

(iii) providing said second population of polynucleotide probes, each comprising a DNA fragment from the modified host genome, suspected to contain said foreign DNA, and having a second, distinguishable label.

9. The method of claim 8, wherein said modified host genome is one of a plurality of transgenic organisms, and the method comprises:

carrying out step (i) for each type of foreign DNA suspected of being present in said plurality of transgenic organisms;

carrying out step (ii) for each different type of unmodified host genome represented in the plurality;

carrying out step (iii) for each transgenic organism of the plurality;

carrying out steps (a) - (d) for each transgenic organism of the plurality, and for each type of foreign DNA suspected of being present in that organism, to determine the presence or absence of foreign DNA in each organism of the plurality; and

selecting one or more of the plurality of transgenic organisms, according to a predetermined selection criterion based on the presence of the foreign DNA in the organism.

10. The method of claim 8, wherein said transgenic organisms are transgenic plant lines.

11. A kit for use in detecting foreign DNA in a modified host genome, by competitive hybridization of probes to a reference library, the kit comprising:

(i) a reference nucleic acid library containing DNA sequences characteristic of said foreign DNA, wherein different sequences are attached to separate solid phase supports in clonal subpopulations;

(ii) a first plurality of probes, derived from a nucleic acid library from the unmodified host genome, not containing said foreign DNA, and having a first label, and

(iii) a second plurality of probes, derived from a nucleic acid library from the modified host genome, suspected of containing said foreign DNA, and having a second label distinguishable from said first label.

12. The kit of claim 11, wherein said probes have a length such that some portion of the first population of probes are able to hybridize with sequences of the reference DNA population under conditions of said hybridization.